```
Title:            US-10-666-513-2
Perfect score:    259
Sequence:         1 TKLEDHLEGIINIGHQYSVR..........ELKQLGTKELPKTLQNXKDQ 50

Scoring table:    BLOSUM62
                  Gapop 10.0 , Gapext 0.5

Searched:         2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters:      2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       A_Geneseq_23Sep04:*
                 1:  geneseqp1980s:*
                 2:  geneseqp1990s:*
                 3:  geneseqp2000s:*
                 4:  geneseqp2001s:*
                 5:  geneseqp2002s:*
                 6:  geneseqp2003as:*
                 7:  geneseqp2003bs:*
                 8:  geneseqp2004s:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	257	99.2	50	3	AAY90763	Aay90763 Human EN-
2	230	88.8	90	3	AAY90765	Aay90765 Bovine CA
3	230	88.8	90	3	AAY90764	Aay90764 Bovine co
4	230	88.8	92	2	AAW03563	Aaw03563 Calcium b
5	206	79.5	91	2	AAW01826	Aaw01826 Component
6	206	79.5	91	2	AAW93819	Aaw93819 Angiotrop
7	189	73.0	91	4	AAB31909	Aab31909 Amino aci
8	189	73.0	92	2	AAW03564	Aaw03564 Calcium b
9	189	73.0	92	2	AAW24137	Aaw24137 Human che
10	189	73.0	92	3	AAB45542	Aab45542 Human S10
11	189	73.0	92	4	AAB31911	Aab31911 Amino aci
12	189	73.0	92	4	AAB31907	Aab31907 Amino aci
13	189	73.0	92	4	AAB31908	Aab31908 Amino aci
14	189	73.0	92	7	ADA93649	Ada93649 Human cal
15	189	73.0	92	8	ADN04192	Adn04192 Antipsori
16	189	73.0	92	8	ADO19540	Ado19540 Human PRO
17	174	67.2	95	4	ABG27582	Abg27582 Novel hum
18	172	66.4	46	4	ABB43183	Abb43183 Peptide #
19	172	66.4	46	4	AAM37021	Aam37021 Peptide #
20	172	66.4	46	4	ABB26281	Abb26281 Protein #

21	172	66.4	46	4	AAM76914	Aam76914 Human bon
22	172	66.4	46	4	AAM64093	Aam64093 Human bra
23	172	66.4	46	4	ABG58579	Abg58579 Human liv
24	172	66.4	46	5	ABG46027	Abg46027 Human pep
25	139	53.7	30	2	AAR85169	Aar85169 Bovine se
26	114	44.0	112	7	ADB79921	Adb79921 Rat intra
27	114	44.0	112	7	ADE57108	Ade57108 Rat Prote
28	114	44.0	113	6	ABU63335	Abu63335 Rat intra
29	110	42.5	114	2	AAW17062	Aaw17062 Human mul
30	110	42.5	114	2	AAW60178	Aaw60178 Human cal
31	110	42.5	114	2	AAY48615	Aay48615 Human bre
32	110	42.5	114	3	AAY87637	Aay87637 Human cal
33	110	42.5	114	3	AAB45539	Aab45539 Human S10
34	110	42.5	114	4	ABB44613	Abb44613 Human wou
35	110	42.5	114	4	AAB31905	Aab31905 Amino aci
36	110	42.5	114	6	ABB82712	Abb82712 Human MRP
37	110	42.5	114	7	ADB17567	Adb17567 Human mye
38	110	42.5	114	7	ADE57110	Ade57110 Human Pro
39	110	42.5	114	7	ADE34548	Ade34548 Human mig
40	110	42.5	114	7	ADF09358	Adf09358 Human cal
41	110	42.5	114	8	ADL83164	Adl83164 Human PRO
42	110	42.5	114	8	ADN03968	Adn03968 Antipsori
43	110	42.5	114	8	ADQ30562	Adq30562 Pancreas
44	110	42.5	115	4	AAB31930	Aab31930 Amino aci
45	110	42.5	152	4	AAM39994	Aam39994 Human pol

```
Title:            US-10-666-513-2
Perfect score:    259
Sequence:         1 TKLEDHLEGIINIGHQYSVR.........ELKQLGTKELPKTLQNXKDQ 50


Scoring table:    BLOSUM62
                  Gapop 10.0 , Gapext 0.5


Searched:         478139 seqs, 66318000 residues


Total number of hits satisfying chosen parameters:      478139


Minimum DB seq length: 0
Maximum DB seq length: 2000000000


Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries


Database :       Issued_Patents_AA:*
                 1:  /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
                 2:  /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
                 3:  /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
                 4:  /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
                 5:  /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                 6:  /cgn2_6/ptodata/1/iaa/backfiles1.pep:*


       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
       and is derived by analysis of the total score distribution.
```

<div align="center">SUMMARIES</div>

Result No.	Score	% Query Match	Length	DB	ID	Description
1	257	99.2	50	4	US-09-263-312-2	Sequence 2, Appli
2	257	99.2	50	4	US-09-826-589-2	Sequence 2, Appli
3	230	88.8	51	2	US-08-568-310D-2	Sequence 2, Appli
4	230	88.8	51	3	US-09-270-455-2	Sequence 2, Appli
5	230	88.8	90	4	US-09-263-312-3	Sequence 3, Appli
6	230	88.8	90	4	US-09-826-589-3	Sequence 3, Appli
7	230	88.8	90	4	US-09-826-589-4	Sequence 4, Appli
8	230	88.8	92	2	US-08-568-310D-19	Sequence 19, Appl
9	230	88.8	92	3	US-09-270-455-19	Sequence 19, Appl
10	206	79.5	91	3	US-08-794-000-2	Sequence 2, Appli
11	206	79.5	91	4	US-09-646-651C-1	Sequence 1, Appli
12	189	73.0	92	2	US-08-568-310D-20	Sequence 20, Appl
13	189	73.0	92	3	US-09-270-455-20	Sequence 20, Appl
14	114	44.0	113	2	US-08-918-727-7	Sequence 7, Appli
15	114	44.0	113	3	US-09-205-680A-7	Sequence 7, Appli
16	110	42.5	50	1	US-08-200-016-5	Sequence 5, Appli
17	110	42.5	109	1	US-07-987-272A-8	Sequence 8, Appli
18	110	42.5	114	1	US-08-385-241-3	Sequence 3, Appli
19	110	42.5	114	4	US-09-214-272-4	Sequence 4, Appli
20	110	42.5	114	4	US-09-806-382A-4	Sequence 4, Appli
21	87	33.6	74	4	US-09-513-999C-5490	Sequence 5490, Ap
22	87	33.6	95	4	US-09-919-172-102	Sequence 102, App

23	87	33.6	95	4	US-09-976-594-467	Sequence 467, App
24	84	32.4	91	1	US-07-987-272A-11	Sequence 11, Appl
25	84	32.4	92	2	US-08-918-727-5	Sequence 5, Appli
26	84	32.4	92	2	US-09-051-589-1	Sequence 1, Appli
27	84	32.4	92	3	US-09-205-680A-5	Sequence 5, Appli
28	84	32.4	92	4	US-09-919-039-184	Sequence 184, App
29	83	32.0	101	1	US-08-190-560-2	Sequence 2, Appli
30	83	32.0	101	1	US-08-469-277-2	Sequence 2, Appli
31	83	32.0	101	2	US-08-468-946-2	Sequence 2, Appli
32	83	32.0	101	2	US-08-468-942-2	Sequence 2, Appli
33	83	32.0	101	4	US-09-298-625-2	Sequence 2, Appli
34	75	29.0	45	1	US-08-056-200-98	Sequence 98, Appl
35	75	29.0	45	2	US-08-800-644-98	Sequence 98, Appl
36	75	29.0	107	4	US-09-513-999C-5491	Sequence 5491, Ap
37	74	28.6	45	1	US-08-056-200-101	Sequence 101, App
38	74	28.6	45	2	US-08-800-644-101	Sequence 101, App
39	74	28.6	47	1	US-08-200-016-2	Sequence 2, Appli
40	74	28.6	93	1	US-07-987-272A-7	Sequence 7, Appli
41	74	28.6	93	1	US-07-987-272A-16	Sequence 16, Appl
42	74	28.6	93	1	US-08-385-241-1	Sequence 1, Appli
43	74	28.6	93	4	US-09-214-272-2	Sequence 2, Appli
44	74	28.6	93	4	US-09-806-382A-3	Sequence 3, Appli
45	73	28.2	45	1	US-08-056-200-97	Sequence 97, Appl

```
Title:            US-10-666-513-2
Perfect score:    259
Sequence:         1 TKLEDHLEGIINIGHQYSVR.........ELKQLGTKELPKTLQNXKDQ 50


Scoring table:    BLOSUM62
                  Gapop 10.0 , Gapext 0.5


Searched:         1608061 seqs, 361289386 residues


Total number of hits satisfying chosen parameters:        1608061


Minimum DB seq length: 0
Maximum DB seq length: 2000000000


Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries


Database :        Published_Applications_AA:*
                  1:  /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
                  2:  /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
                  3:  /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
                  4:  /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
                  5:  /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
                  6:  /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
                  7:  /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
                  8:  /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
                  9:  /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
                  10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
                  11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
                  12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
                  13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
                  14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
                  15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
                  16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
                  17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
                  18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
                  19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
                  20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	257	99.2	50	9	US-09-826-589-2	Sequence 2, Appli
2	257	99.2	50	9	US-09-872-185B-9	Sequence 9, Appli
3	257	99.2	50	15	US-10-666-513-2	Sequence 2, Appli
4	257	99.2	50	16	US-10-665-867-2	Sequence 2, Appli
5	230	88.8	90	9	US-09-826-589-3	Sequence 3, Appli
6	230	88.8	90	9	US-09-826-589-4	Sequence 4, Appli
7	230	88.8	90	9	US-09-872-185B-11	Sequence 11, Appl
8	230	88.8	90	9	US-09-872-185B-12	Sequence 12, Appl

9	230	88.8	90	15	US-10-666-513-3	Sequence 3, Appli
10	230	88.8	90	16	US-10-665-867-3	Sequence 3, Appli
11	230	88.8	90	16	US-10-665-867-4	Sequence 4, Appli
12	189	73.0	92	14	US-10-077-600-2	Sequence 2, Appli
13	189	73.0	92	16	US-10-755-889-334	Sequence 334, App
14	172	66.4	46	9	US-09-864-761-41579	Sequence 41579, A
15	114	44.0	112	14	US-10-205-219-161	Sequence 161, App
16	114	44.0	113	10	US-09-492-026-7	Sequence 7, Appli
17	110	42.5	114	9	US-09-214-272-4	Sequence 4, Appli
18	110	42.5	114	14	US-10-134-841-4	Sequence 4, Appli
19	110	42.5	114	14	US-10-308-279-32	Sequence 32, Appl
20	110	42.5	114	14	US-10-116-275-225	Sequence 225, App
21	110	42.5	114	14	US-10-131-410-146	Sequence 146, App
22	110	42.5	114	15	US-10-424-599-159736	Sequence 159736,
23	110	42.5	114	16	US-10-755-889-330	Sequence 330, App
24	110	42.5	114	17	US-10-733-969A-49	Sequence 49, Appl
25	109	42.1	44	9	US-09-864-761-41096	Sequence 41096, A
26	104	40.2	44	10	US-09-877-843-84	Sequence 84, Appl
27	89	34.4	101	9	US-09-393-433-2	Sequence 2, Appli
28	89	34.4	101	9	US-09-781-509-2	Sequence 2, Appli
29	89	34.4	101	14	US-10-269-643-2	Sequence 2, Appli
30	89	34.4	119	13	US-10-087-192-1155	Sequence 1155, Ap
31	87	33.6	95	9	US-09-919-172-102	Sequence 102, App
32	87	33.6	95	9	US-09-981-353-98	Sequence 98, Appl
33	87	33.6	95	17	US-10-752-986-102	Sequence 102, App
34	87	33.6	113	15	US-10-276-774-2377	Sequence 2377, Ap
35	84	32.4	66	15	US-10-336-603A-104	Sequence 104, App
36	84	32.4	92	10	US-09-492-026-5	Sequence 5, Appli
37	84	32.4	92	10	US-09-919-039-184	Sequence 184, App
38	84	32.4	92	15	US-10-336-603A-102	Sequence 102, App
39	84	32.4	97	16	US-10-363-829-412	Sequence 412, App
40	84	32.4	101	17	US-10-425-115-219479	Sequence 219479,
41	83	32.0	92	17	US-10-425-115-236005	Sequence 236005,
42	83	32.0	101	9	US-09-393-433-1	Sequence 1, Appli
43	83	32.0	101	9	US-09-781-509-1	Sequence 1, Appli
44	83	32.0	101	13	US-10-067-618-2	Sequence 2, Appli
45	83	32.0	101	13	US-10-135-152-2	Sequence 2, Appli

Title: US-10-666-513-2
Perfect score: 259
Sequence: 1 TKLEDHLEGIINIGHQYSVR.........ELKQLGTKELPKTLQNXKDQ 50

Scoring table: BLOSUM62
                  Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR_79:*
                  1: pir1:*
                  2: pir2:*
                  3: pir3:*
                  4: pir4:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                        %
Result   Query
   No.   Score   Match Length DB   ID   Description
   ----
       1   206   79.5   91   2   A55406   calgranulin c - pi
       2   189   73.0   92   2   JC4712   S-100 calcium-bind
       3   131   50.6   122   1   A42628   calgranulin B - bo
       4   114   44.0   113   1   JN0686   calgranulin B - ra
       5   110   42.5   114   1   B31848   calgranulin B [val
       6   89   34.4   101   2   S06207   calvasculin - mous
       7   87   33.6   95   2   S24146   S-100 protein P -
       8   87   33.6   101   2   S01759   calvasculin - rat
       9   84   32.4   92   1   BCHUIB   S-100 protein beta
      10   84   32.4   92   2   A48015   S-100 protein beta
      11   84   32.4   92   2   A26557   S-100 protein beta
      12   83   32.0   91   1   BCBOIB   S-100 protein beta
      13   83   32.0   100   2   A53217   placental calcium-
      14   83   32.0   101   2   A48219   calvasculin - huma
      15   81   31.3   591   2   A45135   profilaggrin - hum
      16   78   30.1   113   1   S68242   calgranulin B - mo
      17   77   29.7   306   2   A48118   major epidermal ca
      18   74   28.6   93   1   BCHUCF   calgranulin A [val
      19   73   28.2   89   1   I56163   calgranulin A - mo
      20   72   27.8   95   1   S35985   S-100 protein alph
      21   71   27.4   94   1   BCBOIA   S-100 protein alph
      22   71   27.4   94   1   BCHUIA   S-100 protein alph
      23   70   27.0   89   1   JN0685   calgranulin A - ra
      24   69.5   26.8   110   2   B48219   S-100 calcium-bind

25	68	26.3	90	1	BCHUY	calcyclin - human
26	68	26.3	98	2	JC5064	S-100 calcium-bind
27	68	26.3	98	2	JC5065	calcium-binding pr
28	67	25.9	90	1	S27011	calcyclin - rabbit
29	67	25.9	98	2	A41988	S-100 calcium-bind
30	65	25.1	217	2	JE0330	26-kDa Ca2+-bindin
31	64	24.7	89	2	A54314	calcyclin - mouse
32	64	24.7	90	2	B28363	calcyclin - rat
33	64	24.7	279	2	AI1012	hypothetical prote
34	63.5	24.5	876	2	G89952	DNA polymerase I [
35	63	24.3	102	1	JQ1300	calgizzarin - rabb
36	61.5	23.7	310	2	AG1733	gp49 (Bacteriophag
37	61	23.6	97	2	A30129	S-100 protein, lun
38	61	23.6	469	2	S55167	IME2-dependent sig
39	60.5	23.4	97	1	JH0663	calpactin I light
40	60.5	23.4	438	2	H72241	fixC protein - The
41	58.5	22.6	97	2	A28489	calpactin I light
42	57.5	22.2	283	2	G83754	transcription regu
43	57.5	22.2	455	2	E90316	oxidoreductase [im
44	57.5	22.2	757	2	B90572	lipoprotein [impor
45	57.5	22.2	2108	2	S28417	CDC39 protein - ye

Title: US-10-666-513-2
Perfect score: 259
Sequence: 1 TKLEDHLEGIINIGHQYSVR..........ELKQLGTKELPKTLQNXKDQ 50

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181.

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   UniProt_02:*
                1: uniprot_sprot:*
                2: uniprot_trembl:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	230	88.8	70	2	Q9TR16	Q9tr16 bos taurus
2	230	88.8	91	1	S112_BOVIN	P79105 bos taurus
3	206	79.5	91	1	S112_PIG	P80310 sus scrofa
4	189	73.0	91	1	S112_HUMAN	P80511 homo sapien
5	189	73.0	92	2	AAH70294	Aah70294 homo sapi
6	136	52.5	81	1	S112_RABIT	O77791 oryctolagus
7	133	51.4	122	1	S109_BOVIN	P28783 bos taurus
8	114	44.0	111	2	Q761U7	Q761u7 rattus norv
9	114	44.0	111	2	BAC82423	Bac82423 rattus no
10	114	44.0	112	1	S109_RAT	P50116 rattus norv
11	110	42.5	114	1	S109_HUMAN	P06702 homo sapien
12	98	37.8	119	2	Q6PRV2	Q6prv2 coturnix co
13	98	37.8	119	2	AAT01286	Aat01286 coturnix
14	94	36.3	118	1	·S109_RABIT	P50117 oryctolagus
15	94	36.3	119	1	M126_CHICK	P28318 gallus gall
16	91	35.1	100	2	Q7ZVA4	Q7zva4 brachydanio
17	90	34.7	101	2	O93395	O93395 salvelinus
18	89	34.4	101	1	S104_MOUSE	P07091 mus musculu
19	89	34.4	101	2	BAB22543	Bab22543 mus muscu
20	87.5	33.8	2850	1	HORN_HUMAN	Q86yz3 homo sapien
21	87	33.6	95	1	S10P_HUMAN	P25815 homo sapien
22	87	33.6	95	2	AAO41114	Aao41114 homo sapi
23	87	33.6	95	2	AAP35953	Aap35953 homo sapi
24	87	33.6	101	1	S104_RAT	P05942 rattus norv
25	85	32.8	92	2	Q925T3	Q925t3 cricetulus
26	84	32.4	91	1	S10B_HUMAN	P04271 homo sapien

27	84	32.4	91	1	S10B_MOUSE	P50114 mus musculu
28	84	32.4	91	1	S10B_RAT	P04631 rattus norv
29	84	32.4	92	2	Q6YNR6	Q6ynr6 oryctolagus
30	84	32.4	92	2	AAL12231	Aal12231 oryctolag
31	84	32.4	92	2	AAH61178	Aah61178 mus muscu
32	84	32.4	95	2	Q6DGT8	Q6dgt8 brachydanio
33	83	32.0	91	1	S10B_BOVIN	P02638 bos taurus
34	83	32.0	100	1	S104_BOVIN	P35466 bos taurus
35	83	32.0	101	1	S104_HUMAN	P26447 homo sapien
36	83	32.0	101	2	CAG29341	Cag29341 homo sapi
37	81	31.3	591	2	Q01720	Q01720 homo sapien
38	81	31.3	687	2	Q9H4U2	Q9h4u2 homo sapien
39	78	30.1	112	1	S109_MOUSE	P31725 mus musculu
40	77	29.7	1218	2	Q05331	Q05331 homo sapien
41	75	29.0	148	2	Q8BLX1	Q8blx1 mus musculu
42	75	29.0	2496	1	HORN_MOUSE	Q8vhd8 mus musculu
43	74	28.6	93	1	S108_HUMAN	P05109 h calgranul
44	74	28.6	93	2	AAP36042	Aap36042 homo sapi
45	74	28.6	93	2	CAG28602	Cag28602 homo sapi